

10/568332

61310.us.sequence
SEQUENCE LISTING
AP20 Record 10 13 FEB 2006

<110> Stempfer, Gunter
Alliger, Peter
Palma, Norbert

<120> Process for the purification of recombinant polypeptides

<130> BP/G-33315A LNG 61310.US

<150> PCT/EP2004/009055

<151> 2004-08-12

<150> US 60/494,915

<151> 2003-08-13

<160> 14

<170> PatentIn version 3.3

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ggttcgtacg cgccgcctac aagtgggtat ctagggaaac gttccggggg cgtcgctgca		180
acggcggtctc cggatctggg tgagagggga aatccatgtc gagagttctg caccggcgg		240
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			Met	Leu	Arg	Val	Leu	His	Arg	Ala						
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gcg	tcc	gcc	ttg	gtt	atg	gct	act	gtg	atc	ggc	ctt	gct	ccc	gct	gtc	281
Ala	Ser	Ala	Leu	Val	Met	Ala	Thr	Val	Ile	Gly	Leu	Ala	Pro	Ala	Val	
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Ala	Phe	Ala	Cys	Asp	Leu	Pro	Gln	Thr	His	Ser	Leu	Gly	Ser	Arg	Arg	
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acc	ttg	atg	ctt	ctg	gca	cag	atg	cg	cga	atc	tct	ctt	ttc	tct	tgc	377
Thr	Leu	Met	Leu	Leu	Ala	Gln	Met	Arg	Arg	Ile	Ser	Leu	Phe	Ser	Cys	
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tta	aag	gat	cga	cat	gac	ttc	ggt	ttc	ccg	cag	gag	gag	ttc	ggt	aac	425
Leu	Lys	Asp	Arg	His	Asp	Phe	Gly	Phe	Pro	Gln	Glu	Glu	Phe	Gly	Asn	
					60			65		70						
cag	ttc	caa	aag	gct	gaa	acc	atc	ccg	gta	ttg	cat	gag	atg	atc	cag	473
Gln	Phe	Gln	Lys	Ala	Glu	Thr	Ile	Pro	Val	Leu	His	Glu	Met	Ile	Gln	
					75			80		85						
cag	atc	ttc	aac	ctg	ttc	agc	act	aag	gac	tct	tct	gct	gct	tgg	gat	521
Gln	Ile	Phe	Asn	Leu	Phe	Ser	Thr	Lys	Asp	Ser	Ser	Ser	Ala	Ala	Trp	Asp
					90			95		100						
gag	acc	ctg	ctt	gac	aaa	ttc	tac	act	gaa	ctg	tac	cag	cag	ctg	aac	569
Glu	Thr	Leu	Leu	Asp	Lys	Phe	Tyr	Thr	Glu	Leu	Tyr	Gln	Gln	Leu	Asn	
105					110				115					120		
gac	ctg	gaa	gcc	tgc	gtg	atc	cag	ggt	gtg	ggt	gtg	act	gag	act	ccg	617
Asp	Leu	Glu	Ala	Cys	Val	Ile	Gln	Gly	Val	Gly	Val	Thr	Glu	Thr	Pro	
					125				130			135				
ctg	atg	aag	gag	gac	tct	att	ctg	gct	gtg	cga	aaa	tac	ttc	caa	ccg	665

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Leu Met Lys Glu Asp Ser Ile Leu Ala Val Arg Lys Tyr Phe Gln Arg
 140 145 150

atc act ctg tat ctg aaa gag aag aaa tac agc ccg tgc gcc tgg gag 713
 Ile Thr Leu Tyr Leu Lys Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu
 155 160 165

gtt gtc cga gca gaa atc atg cggtcttttttttacc aac ttg 761
 Val Val Arg Ala Glu Ile Met Arg Ser Phe Ser Leu Ser Thr Asn Leu
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caa gaa tct tta cga agc aag gaa taa tacgcgtact agtgaattc 807
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 35 40 45

Arg Arg Ile Ser Leu Phe Ser Cys Leu Lys Asp Arg His Asp Phe Gly
 50 55 60

Phe Pro Gln Glu Glu Phe Gly Asn Gln Phe Gln Lys Ala Glu Thr Ile
 65 70 75 80

Pro Val Leu His Glu Met Ile Gln Gln Ile Phe Asn Leu Phe Ser Thr
 85 90 95

Lys Asp Ser Ser Ala Ala Trp Asp Glu Thr Leu Leu Asp Lys Phe Tyr
 100 105 110

Thr Glu Leu Tyr Gln Gln Leu Asn Asp Leu Glu Ala Cys Val Ile Gln
 115 120 125

Gly Val Gly Val Thr Glu Thr Pro Leu Met Lys Glu Asp Ser Ile Leu
 130 135 140

Ala Val Arg Lys Tyr Phe Gln Arg Ile Thr Leu Tyr Leu Lys Glu Lys
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145

150

155

160

Lys Tyr Ser Pro Cys Ala Trp Glu Val Val Arg Ala Glu Ile Met Arg
165 170 175

Ser Phe Ser Leu Ser Thr Asn Leu Gln Glu Ser Leu Arg Ser Lys Glu
180 185 190